



RAW SEQUENCE LISTING

DATE: 06/27/2002

PATENT APPLICATION: US/09/899,634B

TIME: 13:06:28

Input Set : A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt

Output Set: N:\CRF3\06272002\I899634B.raw

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3 <110> APPLICANT: Thomas Buhler; Reto Andreas Gadiant; Reinhard Korn; Rao Movva
5 <120> TITLE OF INVENTION: pCAR and its uses
7 <130> FILE REFERENCE: 4-31499A
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/899,634B
C--> 9 <141> CURRENT FILING DATE: 2002-06-17
9 <160> NUMBER OF SEQ ID NOS: 12
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 4286
15 <212> TYPE: DNA
C--> 16 <213> ORGANISM: Artificial/Unknown
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (3229)..(4014)
21 <223> OTHER INFORMATION: delta pCAR gene
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29 agttgggatc tttgcattgg cccacggctc tcaggatggg gatgctcccc ttcagcaccc      180
31 ggttcccctt ggaaactgat ggtcctggct ctgtggcatg gcagtggcac tgtgaggagc      240
33 ccctaccagc agcacacagt gggtttggca ctgccacgct ccgcatgccg cgctctgatc      300
35 caaccccata atcaaggga cccgaattgc cccatcattg cccccaccac cccatcctg      360
37 ccggggccctc acaccccaag ctgccttggt gtgacattcc ccagcccaaa cccacggctt      420
39 catggctacc gcggggcatt tccattgcc gccccattat cagctctgca cacctccgc      480
41 tgtacccatg cctcgtggct gcccttcttt gacgtataat cttctaatta ataccgggc      540
43 ttgtcaaagt ggagcaciaa cgttaattaa ttcccagca ggcaggtaat taacagtgtg      600
45 actccctttt tgctgcgagt ggggctgata cagagagatg tggcactatg gagcccacgg      660
47 ggtcctggca ctgggtgccc acggaggctc ccatgtgctg cagtgtcacc gcctccgagg      720
49 tgacagtatt gtccctgcgg tgcctctgca gctcagctct gtccacaggg ccacctccag      780
51 tttggagggg acacaatgca gccccgatgc aaccatcct cgcagcatcc cagggacaaa      840
53 gacccactg caagaccgca cacagggtcg ggtcccgtc ccctaataatc tacagtgtt      900
55 ttgcatggcc ccttaatcaa tgcagttaat cagcatgcgc tcatgcaccg ctctggagct      960
57 gcaaaagccc tcgcagcgt gtcaccaaac accgcgcacc gccccggccc agcctgcagc     1020
59 acgcgctgca aacaggaaa aaacaaaata ttgccaaat gtaggcaaag gcattcggct      1080
61 gccttgacct ccgcggggcc gggccctgcc tgactcagct ccttactcag cgctcgcttc      1140
63 ctccctccgg ctgccaccgc cgcagcgcac accctgacaa agagtggccc ttaacgggct      1200
65 ctgaggtgca ccagcagtg cactcagcag tccaagggcc ggctggagg tttgcaccgc      1260
67 tacgtgctga cattagcatt gaacttgccc ctgggtagt ctgcaggccg ggcgggtgga      1320
69 gtgtagagag tgcagcgcgc gttgcaccgc gtgccccttc cctcccttg catcccagca      1380
71 ggctgcaccc cagcaccagg cccgtgcatg catgctcctg gtgttattgc agcctggtgc      1440
73 atgcatgcgt cttagtgggt cagcgtgtgt catgcaccc ctttggtgtg tagcagctta      1500
75 gtgcatgcat acccctcggg gttattgctg ctctgtgcac gcacgctcat tgtatcactt      1560
77 catcccagtg catgcactca cactggagcg attgctgctc ggtgcacgca cactcattgt      1620

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79 atcacgtcag ctacgtggct gcacgcacac cgggtgttatt gctgctcggt gcgtgcatgc 1680
81 acatcagtgt cgctgcagct cagtgcattg accatcgcta tccctgcctc 1740
83 tcctgctggc gctccccggg aggtgacttc aaggggaccg caggaccacc tcgggggttg 1800
85 ggggagggct gcacacgcgg acccgcctcc ccctcccaa caaagcactg tggaatcaaa 1860
87 aaggggggag ggggggatgga ggggcgcgtc acaccccgcc cccacaccct cacctcgagg 1920
89 tgagccccac gttctgcttc actctcccca tctccccccc ctccccaccc ccaattttgt 1980
91 atttatttat tttttaatta ttttgtcag cgatgggggc gggggggggg ggggcgcgcg 2040
93 ccaggcgggg cggggcgggg cgaggggcgg ggcggggcga ggcggagagg tgcggcggca 2100
95 gccaatcaga gcgcgcgcgt ccgaaagttt ccttttatgg cgaggcggcg gcggcggcgg 2160
97 ccctataaaa agcgaagcgc gcggcggggc ggagtcgctg cgttgccctc gccccgtgcc 2220
99 ccgctccgcg ccgcctcgcg ccgcgcgcgc cggctctgac tgaccgcgtt actccacag 2280
101 gtgagcgggc gggacggccc ttctcctccg ggctgtaatt agcgtttggt ttaatgacgg 2340
103 ctcgtttctt ttctgtggct gcgtgaaagc cttaaagggc tccgggaggg ccctttgtgc 2400
105 gggggggagc ggctcggggg gtgctgctgc gtgtgtgtgc gtggggagcg ccgcgtgcgg 2460
107 ccgcgcctgc ccggcggctg tgagcgcctg gggcgcggcg cggggctttg tgcctcgc 2520
109 gtgtgcgcga ggggagcgcg gccggggggc gtgccccgcg gtgcgggggg gctgcgaggg 2580
111 gaacaaagcg tgcgtgcggg gtgtgtgcgt gggggggtga gcagggggtg tgggcgcggc 2640
113 ggtcgggctg taaccccccc ctgcaccccc ctccccaggt tgcctgagcag ggcccggtt 2700
115 cgggtgcggg gctccgtgcg gggcgtggcg cggggctcgc cgtgccgggc ggggggtggc 2760
117 ggcaggtggg ggtgccgggc ggggcggggc cgcctcgggc cggggagggc tcgggggagg 2820
119 ggcgcggcgg ccccgaggcg ccggcggctg tcgaggcgcg gcgagccgca gccattgcct 2880
121 tttatggtaa tcgtgcgaga gggcgcaggg acttcctttg tcccaaattc ggcggagccg 2940
123 aaatctggga ggcgcgcgcg caccacctct agcgggcgcg ggcgaagcgg tgcggcgcg 3000
125 gcaggaagga aatgggcggg gagggccttc gtgcgtgcgc gcgccgcgct ccccttctcc 3060
127 atctccagcc tcggggctgc cgcaggggga cggctgcctt cggggggggc ggggcagggc 3120
129 ggggttcggc ttctggcgtg tgaccggcgg ggtttatata ttcccttctc tgttctcgcg 3180
131 cagcccccaa gcttaaggtg cacggcccac gtggggacta gtgccacc atg gcg ctc 3237
132 Met Ala Leu
133 1
135 ctg ctg tgc ttc gtg ctc ctg tgc gga gtc gcg gat ctc acc aga agt 3285
136 Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu Thr Arg Ser
137 5 10 15
139 ttg agt atc act act cct gaa cag atg att gaa aag gcc aaa ggg gaa 3333
140 Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala Lys Gly Glu
141 20 25 30 35
143 act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa gac cag ggg 3381
144 Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu Asp Gln Gly
145 40 45 50
147 ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat cag aag gtg 3429
148 Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn Gln Lys Val
149 55 60 65
151 gat caa gtg att att tta tat tct gga gac aaa att tat gac gac tac 3477
152 Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr Asp Asp Tyr
153 70 75 80
155 tac caa gat ctg aaa gga cga gta cat ttt aca agt aat gat ctc aaa 3525
156 Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn Asp Leu Lys
157 85 90 95
159 tca ggt gat gca tca ata aat gta aca aat cta cag ttg tca gat att 3573
160 Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu Ser Asp Ile

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```

161 100          105          110          115
163 ggc aca tat cag tgc aaa gtg aaa aag gct cct ggt gtt gga aat aag      3621
164 Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val Gly Asn Lys
165          120          125          130
167 aag att cag ctg aca gtt ctt ctt aag cct tca ggt aca aga tgt tat      3669
168 Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr Arg Cys Tyr
169          135          140          145
171 gtt gat gga tca gaa gaa att gga aat gac ttt aaa cta aaa tgt gaa      3717
172 Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu Lys Cys Glu
173          150          155          160
175 cca aaa gaa ggt tca ctc cca tta cta tat gaa tgg cag aaa ttg tcc      3765
176 Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln Lys Leu Ser
177          165          170          175
179 aat tca cag aag ctg ccc acc ttg tgg tta gca gaa atg act tca cct      3813
180 Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met Thr Ser Pro
181 180          185          190          195
183 gtt ata tct gta aaa aat gcc tct act gaa tac tct ggg aca tac agc      3861
184 Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly Thr Tyr Ser
185          200          205          210
187 tgt acc gtg aaa aac aga gtg ggc tct gat cag tgc ctg ctt cgc ctg      3909
188 Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu Leu Arg Leu
189          215          220          225
191 gat gtg gtt cct cct tca aat aga gct gga aca att gca gga gct gtt      3957
192 Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala Gly Ala Val
193          230          235          240
195 ata gga gtt ttg ctt gct cta gtg ctc att ggt ctt atc atc ttt tgc      4005
196 Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile Ile Phe Cys
197          245          250          255
199 tgt cgt taa tctagataag taatgatcat aatcagccat atcacatctg      4054
200 Cys Arg
201 260
203 tagagggtttt acttgcttta aaaaacctcc cacacctccc cctgaacctg aaacataaaa      4114
205 tgaatgcaat tgttggtgtt aacttgctta ttgcagctta taatggttac aaataaagca      4174
207 atagcatcac aaatttcaca aataaagcat ttttttcaact gcattctagt tgtggtttgt      4234
209 ccaaactcat caatgtatct tatcatgtct ggatccccgg gtaccgagct cg      4286
212 <210> SEQ ID NO: 2
213 <211> LENGTH: 261
214 <212> TYPE: PRT
C--> 215 <213> ORGANISM: Artificial/Unknown
W--> 217 <220> FEATURE:
W--> 217 <223> OTHER INFORMATION:
217 <400> SEQUENCE: 2
219 Met Ala Leu Leu Cys Phe Val Leu Leu Cys Gly Val Ala Asp Leu
220 1          5          10          15
223 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
224          20          25          30
227 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
228          35          40          45
231 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn

```

Error

- See explanation p. 6

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232      50              55              60
235 Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser Gly Asp Lys Ile Tyr
236 65              70              75              80
239 Asp Asp Tyr Tyr Gln Asp Leu Lys Gly Arg Val His Phe Thr Ser Asn
240              85              90              95
243 Asp Leu Lys Ser Gly Asp Ala Ser Ile Asn Val Thr Asn Leu Gln Leu
244              100             105             110
247 Ser Asp Ile Gly Thr Tyr Gln Cys Lys Val Lys Lys Ala Pro Gly Val
248              115             120             125
251 Gly Asn Lys Lys Ile Gln Leu Thr Val Leu Leu Lys Pro Ser Gly Thr
252              130             135             140
255 Arg Cys Tyr Val Asp Gly Ser Glu Glu Ile Gly Asn Asp Phe Lys Leu
256 145             150             155             160
259 Lys Cys Glu Pro Lys Glu Gly Ser Leu Pro Leu Leu Tyr Glu Trp Gln
260              165             170             175
263 Lys Leu Ser Asn Ser Gln Lys Leu Pro Thr Leu Trp Leu Ala Glu Met
264              180             185             190
267 Thr Ser Pro Val Ile Ser Val Lys Asn Ala Ser Thr Glu Tyr Ser Gly
268              195             200             205
271 Thr Tyr Ser Cys Thr Val Lys Asn Arg Val Gly Ser Asp Gln Cys Leu
272              210             215             220
275 Leu Arg Leu Asp Val Val Pro Pro Ser Asn Arg Ala Gly Thr Ile Ala
276 225             230             235             240
279 Gly Ala Val Ile Gly Val Leu Leu Ala Leu Val Leu Ile Gly Leu Ile
280              245             250             255
283 Ile Phe Cys Cys Arg
284              260

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287 <210> SEQ ID NO: 3

288 <211> LENGTH: 1098

289 <212> TYPE: DNA

C--> 290 <213> ORGANISM: Artificial/Unknown

292 <220> FEATURE:

293 <221> NAME/KEY: CDS

294 <222> LOCATION: (1)..(1098)

295 <223> OTHER INFORMATION: full length porcine CAR

298 <400> SEQUENCE: 3

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301 1              5              10              15
303 acc aga agt ttg agt atc act act cct gaa cag atg att gaa aag gcc      96
304 Thr Arg Ser Leu Ser Ile Thr Thr Pro Glu Gln Met Ile Glu Lys Ala
305              20              25              30
307 aaa ggg gaa act gcc tat ttg cca tgc aga ttt acc ctg ggt cca gaa      144
308 Lys Gly Glu Thr Ala Tyr Leu Pro Cys Arg Phe Thr Leu Gly Pro Glu
309              35              40              45
311 gac cag ggg ccg ctg gac atc gag tgg ctg ctg tca cca gct gat aat      192
312 Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Leu Ser Pro Ala Asp Asn
313      50              55              60
315 cag aag gtg gat caa gtg att att tta tat tct gga gac aaa att tat      240

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316	Gln	Lys	Val	Asp	Gln	Val	Ile	Ile	Leu	Tyr	Ser	Gly	Asp	Lys	Ile	Tyr	
317	65					70					75				80		
319	gac	gac	tac	tac	caa	gat	ctg	aaa	gga	cga	gta	cat	ttt	aca	agt	aat	288
320	Asp	Asp	Tyr	Tyr	Gln	Asp	Leu	Lys	Gly	Arg	Val	His	Phe	Thr	Ser	Asn	
321					85					90					95		
323	gat	ctc	aaa	tca	ggt	gat	gca	tca	ata	aat	gta	aca	aat	cta	cag	ttg	336
324	Asp	Leu	Lys	Ser	Gly	Asp	Ala	Ser	Ile	Asn	Val	Thr	Asn	Leu	Gln	Leu	
325					100					105					110		
327	tca	gat	att	ggc	aca	tat	cag	tgc	aaa	gtg	aaa	aag	gct	cct	ggt	gtt	384
328	Ser	Asp	Ile	Gly	Thr	Tyr	Gln	Cys	Lys	Val	Lys	Lys	Ala	Pro	Gly	Val	
329					115					120					125		
331	gga	aat	aag	aag	att	cag	ctg	aca	gtt	ctt	ctt	aag	cct	tca	ggt	aca	432
332	Gly	Asn	Lys	Lys	Ile	Gln	Leu	Thr	Val	Leu	Leu	Lys	Pro	Ser	Gly	Thr	
333		130					135					140					
335	aga	tgt	tat	gtt	gat	gga	tca	gaa	gaa	att	gga	aat	gac	ttt	aaa	cta	480
336	Arg	Cys	Tyr	Val	Asp	Gly	Ser	Glu	Glu	Ile	Gly	Asn	Asp	Phe	Lys	Leu	
337	145					150					155					160	
339	aaa	tgt	gaa	cca	aaa	gaa	ggt	tca	ctc	cca	tta	cta	tat	gaa	tgg	cag	528
340	Lys	Cys	Glu	Pro	Lys	Glu	Gly	Ser	Leu	Pro	Leu	Leu	Tyr	Glu	Trp	Gln	
341					165					170						175	
343	aaa	ttg	tcc	aat	tca	cag	aag	ctg	ccc	acc	ttg	tgg	tta	gca	gaa	atg	576
344	Lys	Leu	Ser	Asn	Ser	Gln	Lys	Leu	Pro	Thr	Leu	Trp	Leu	Ala	Glu	Met	
345					180					185					190		
347	act	tca	cct	gtt	ata	tct	gta	aaa	aat	gcc	tct	act	gaa	tac	tct	ggg	624
348	Thr	Ser	Pro	Val	Ile	Ser	Val	Lys	Asn	Ala	Ser	Thr	Glu	Tyr	Ser	Gly	
349					195				200						205		
351	aca	tac	agc	tgt	acc	gtg	aaa	aac	aga	gtg	ggc	tct	gat	cag	tgc	ctg	672
352	Thr	Tyr	Ser	Cys	Thr	Val	Lys	Asn	Arg	Val	Gly	Ser	Asp	Gln	Cys	Leu	
353		210					215					220					
355	ctt	cgc	ctg	gat	gtg	gtt	cct	cct	tca	aat	aga	gct	gga	aca	att	gca	720
356	Leu	Arg	Leu	Asp	Val	Val	Pro	Pro	Ser	Asn	Arg	Ala	Gly	Thr	Ile	Ala	
357	225					230					235					240	
359	gga	gct	gtt	ata	gga	gtt	ttg	ctt	gct	cta	gtg	ctc	att	ggt	ctt	att	768
360	Gly	Ala	Val	Ile	Gly	Val	Leu	Leu	Ala	Leu	Val	Leu	Ile	Gly	Leu	Ile	
361					245					250					255		
363	gtg	ttt	tgc	tgt	cat	aaa	aag	cgc	aga	gaa	gaa	aaa	tac	gaa	aaa	gaa	816
364	Val	Phe	Cys	Cys	His	Lys	Lys	Arg	Arg	Glu	Glu	Lys	Tyr	Glu	Lys	Glu	
365					260					265					270		
367	gtg	cat	cat	gat	atc	agg	gaa	gac	gtg	cct	cct	ccg	aag	agc	aga	acg	864
368	Val	His	His	Asp	Ile	Arg	Glu	Asp	Val	Pro	Pro	Pro	Lys	Ser	Arg	Thr	
369					275					280					285		
371	tcc	act	gcc	aga	agc	tac	ctc	ggc	agc	aac	cac	tcg	tcc	ctg	gga	tcc	912
372	Ser	Thr	Ala	Arg	Ser	Tyr	Leu	Gly	Ser	Asn	His	Ser	Ser	Leu	Gly	Ser	
373					290					295					300		
375	atg	tct	cct	tcc	aac	atg	gaa	ggc	tat	tcc	aag	act	cag	tat	aac	cag	960
376	Met	Ser	Pro	Ser	Asn	Met	Glu	Gly	Tyr	Ser	Lys	Thr	Gln	Tyr	Asn	Gln	
377	305					310					315					320	
379	gta	cca	agc	gaa	gac	ttt	gaa	cgc	gct	cct	cag	agt	cca	act	ctc	ccg	1008
380	Val	Pro	Ser	Glu	Asp	Phe	Glu	Arg	Ala	Pro	Gln	Ser	Pro	Thr	Leu	Pro	

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:2,4

VERIFICATION SUMMARY

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Input Set : A:\20010608 pCAR and its uses seq 1 to seq id 12.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:217 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:217 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:290 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:395 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:397 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:397 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:509 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:524 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:539 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:554 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:569 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:584 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:599 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12